



results of BLAST

BLASTP 2.2.10 [Oct-19-2004]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1105739873-2607-128700542711.BLASTQ4

Query=

(101 letters)

Database: All non-redundant GenBank CDS

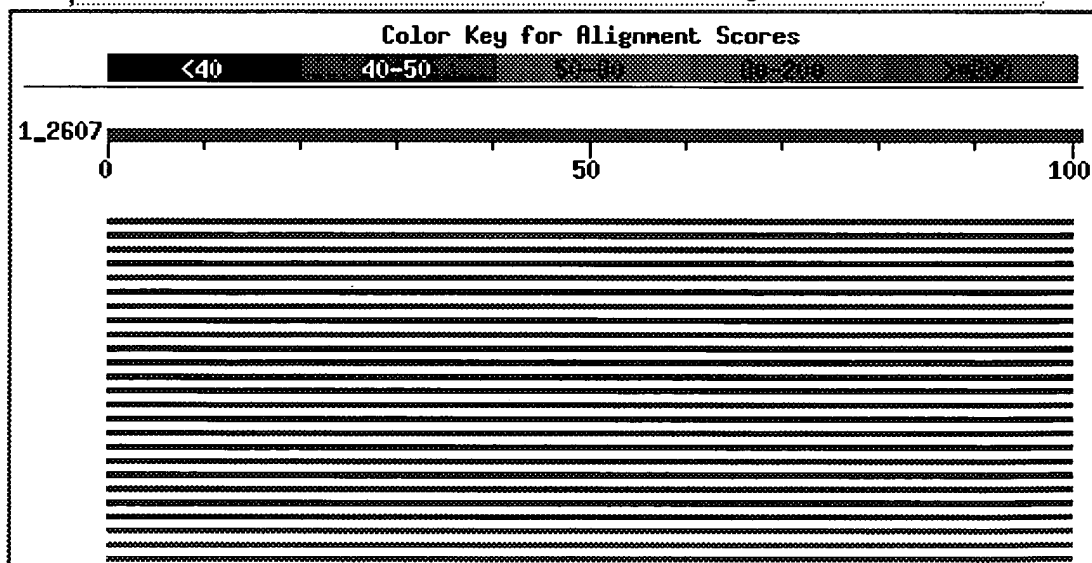
translations+PDB+SwissProt+PIR+PRF excluding environmental samples
2,306,668 sequences; 784,723,489 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 700 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



[Related Structures](#)

Sequences producing significant alignments:

Score E
(bits) Value

gi 15706263 emb CAC69989.1	bromodomain containing 2 [Homo ...	217	6e-56	G
gi 4826806 ref NP_005095.1	bromodomain containing protein ...	217	6e-56	G
gi 1082363 pir A56619	female sterile homeotic (fsh) homolo...	217	6e-56	G
gi 51770504 ref XP_489783.1	similar to MMRING3.1.2 [Mus mu...	217	6e-56	G
gi 57094404 ref XP_532103.1	PREDICTED: similar to Bromodom...	217	6e-56	
gi 47059183 ref NP_997660.1	bromodomain-containing 2 [Ratt...	217	6e-56	G
gi 6753910 ref NP_034368.1	bromodomain containing 2 [Mus m...	217	6e-56	G
gi 55956582 emb CAI11405.1	bromodomain-containing protein ...	217	6e-56	
gi 55725298 emb CAH89514.1	hypothetical protein [Pongo pyg...	217	6e-56	
gi 52545923 emb CAH56179.1	hypothetical protein [Homo sapi...	217	6e-56	
gi 12802525 gb AAK07919.1	ring 3 [Mus musculus]	217	6e-56	G
gi 1370115 emb CAA65450.1	kinase [Homo sapiens]	217	6e-56	G
gi 2995269 emb CAA15818.1	MMRING3.1.1 [Mus musculus]	217	6e-56	G
gi 2780779 db BAA24379.1	Ring3 [Mus musculus] >gi 2780777...	217	6e-56	G
gi 2780775 db BAA24377.1	Ring3 [Mus musculus]	217	6e-56	G
gi 39645317 gb AAH63840.1	BRD2 protein [Homo sapiens]	217	6e-56	G
gi 1588281 prf 2208296A	RING3 protein	217	6e-56	
gi 1370092 emb CAA65449.1	kinase [Gallus gallus]	213	1e-54	
gi 3129967 emb CAA18965.1	RING3 kinase [synthetic construc...	213	1e-54	
gi 34392374 db BAC82511.1	Serine threonine Kinase [Coturn...	213	1e-54	
gi 54311476 gb AAH84758.1	Brd2-A-prov protein [Xenopus lae...	202	2e-51	G
gi 27696271 gb AAH43784.1	Brd2-A-prov protein [Xenopus lae...	202	2e-51	G
gi 50756877 ref XP_415337.1	PREDICTED: similar to RING3 ki...	196	1e-49	G
gi 8575733 gb AAF78072.1	bromodomain-containing FSH-like p...	195	2e-49	G
gi 11067749 ref NP_031397.1	bromodomain containing protein...	195	2e-49	G
gi 34853148 ref XP_342397.1	similar to Brd3 protein [Rattu...	195	2e-49	G
gi 21594670 gb AAH32124.1	BRD3 protein [Homo sapiens] >gi ...	195	2e-49	G
gi 31981064 ref NP_075825.2	bromodomain containing 3 [Mus ...	195	2e-49	G
gi 40788944 db BAA05393.2	KIAA0043 [Homo sapiens]	195	2e-49	G
gi 26345416 db BAC36359.1	unnamed protein product [Mus mu...	195	2e-49	G
gi 47115837 sp Q8K2F0 BRD3_MOUSE	Bromodomain-containing pro...	195	2e-49	G
gi 26332152 db BAC29806.1	unnamed protein product [Mus mu...	195	2e-49	G
gi 50757295 ref XP_425330.1	PREDICTED: similar to bromodom...	193	9e-49	G
gi 47086635 ref NP_997867.1	Unknown (protein for MGC:77289...	191	6e-48	G
gi 33416361 gb AAH55533.1	Zgc:77289 protein [Danio rerio]	191	6e-48	G
gi 33417197 gb AAH55508.1	Unknown (protein for IMAGE:38191...	189	2e-47	
gi 33416865 gb AAH55543.1	Unknown (protein for IMAGE:59138...	188	3e-47	
gi 19171509 emb CAC84085.1	hypothetical protein [Takifugu ...	187	7e-47	
gi 47216871 emb CAG11678.1	unnamed protein product [Tetrao...	186	2e-46	
gi 47212213 emb CAF94980.1	unnamed protein product [Tetrao...	184	4e-46	
gi 7657218 ref NP_055114.1	bromodomain-containing protein ...	182	2e-45	G
gi 33879612 gb AAH30158.1	BRD4 protein [Homo sapiens]	182	2e-45	G
gi 34862361 ref XP_343176.1	similar to bromodomain-contain...	182	2e-45	G
gi 37674287 ref NP_932762.1	bromodomain containing 4 isofo...	182	2e-45	G
gi 31560788 ref NP_065254.2	bromodomain containing 4 isofo...	182	2e-45	G
gi 19718731 ref NP_490597.1	bromodomain-containing protein...	182	2e-45	G
gi 52350614 gb AAH82782.1	Unknown (protein for IMAGE:53893...	182	2e-45	
gi 27804346 gb AAO22237.1	BRD4-NUT fusion oncoprotein [Hom...	182	2e-45	
gi 3184498 gb AAC27978.1	R31546_1 [Homo sapiens]	182	2e-45	G

gi 45501005 qb AAH67129.1	Unknown (protein for IMAGE:61387...	182	2e-45	
gi 50400639 sp Q9ESU6 BRD4 MOUSE	Bromodomain-containing pro...	182	2e-45	G
gi 18157527 db EAB83842.1	BRD2~partially supported by GEN...	182	2e-45	
gi 49118460 qb AAH73443.1	LOC443648 protein [Xenopus laevis]	180	8e-45	G
gi 45554416 ref NP_996370.1	CG2252-PC, isoform C [Drosophi...	180	1e-44	G
gi 24640482 ref NP_511078.2	CG2252-PB, isoform B [Drosophi...	180	1e-44	G
gi 24210305 emb CAD54663.1	bromodomain containing 2 [Danio...	180	1e-44	G
gi 280611 pir A43742	female sterile homeotic protein, 205K...	180	1e-44	
gi 31206311 ref XP_312107.1	ENSANGP00000016848 [Anopheles ...	179	1e-44	G
gi 55241967 qb EAA07774.2	ENSANGP00000016848 [Anopheles ga...	179	1e-44	
gi 47210026 emb CAF90901.1	unnamed protein product [Tetrao...	179	2e-44	
gi 47209011 emb CAF91369.1	unnamed protein product [Tetrao...	179	2e-44	
gi 57092013 ref XP_537803.1	PREDICTED: similar to Bromodom...	177	9e-44	
gi 49899749 qb AAH76786.1	Brd4-prov protein [Xenopus laevis]	176	1e-43	G
gi 48134425 ref XP_393347.1	similar to ENSANGP00000016848 ...	176	1e-43	G
gi 28278510 qb AAH45866.1	Similar to bromodomain containin...	176	2e-43	
gi 10441758 qb AAG17179.1	RING3 [Myxine glutinosa]	174	4e-43	
gi 20302741 qb AAM18869.1	unknown [Branchiostoma floridae]	171	5e-42	
gi 38014413 qb AAH60452.1	LOC398944 protein [Xenopus laevis]	167	9e-41	G
gi 55587546 ref XP_524767.1	PREDICTED: similar to testis-s...	166	1e-40	
gi 28839607 qb AAH47900.1	BRDT protein [Homo sapiens]	166	2e-40	G
gi 33355659 qb AAQ16198.1	testis-specific BRDT protein [Ho...	166	2e-40	G
gi 2554915 qb AAB87862.1	BRDT [Homo sapiens]	166	2e-40	G
gi 46399200 ref NP_997072.1	testis-specific bromodomain pr...	166	2e-40	G
gi 57088245 ref XP_537079.1	PREDICTED: similar to testis-s...	163	1e-39	
gi 38541875 qb AAH62700.1	BRDT protein [Homo sapiens]	162	2e-39	G
gi 16905089 ref NP_473395.1	bromodomain, testis-specific [...	161	4e-39	G
gi 34875962 ref XP_223146.2	similar to bromodomain-contain...	160	7e-39	G
gi 50927337 qb AAH78999.1	Unknown (protein for MGC:93906) ...	160	7e-39	
gi 50751326 ref XP_422346.1	PREDICTED: similar to bromodom...	160	7e-39	G
gi 47208417 emb CAF92198.1	unnamed protein product [Tetrao...	160	1e-38	
gi 52545711 emb CAH56208.1	hypothetical protein [Homo sapi...	130	7e-30	G
gi 55648495 ref XP_512452.1	PREDICTED: similar to bromodom...	128	5e-29	
gi 57101624 ref XP_541985.1	PREDICTED: similar to abhydrol...	127	8e-29	
gi 47210344 emb CAF96012.1	unnamed protein product [Tetrao...	124	5e-28	
gi 1256804 qb AAB18943.1	RING3 protein [Xenopus laevis]	121	4e-27	
gi 25152243 ref NP_509770.2	bromodomain containing (XL193)...	110	1e-23	G
gi 7504519 pir T22845	hypothetical protein F57C7.1a - Caen...	110	1e-23	
gi 2654068 qb AAB87684.1	RING3 [Danio rerio]	107	7e-23	G
gi 39582126 emb CAE60803.1	Hypothetical protein CBG04495 [...	107	1e-22	
gi 24649433 ref NP_651190.1	CG13597-PA [Drosophila melanog...	104	7e-22	G
gi 19528091 qb AAL90160.1	AT24535p [Drosophila melanogaster]	104	7e-22	
gi 17568247 ref NP_509771.1	bromodomain protein (XL193) [C...	103	1e-21	G
gi 32564850 ref NP_871879.1	bromodomain containing protein...	101	5e-21	G
gi 17510957 ref NP_491384.1	bromodomain containing protein...	101	5e-21	G
gi 39598215 emb CAE68907.1	Hypothetical protein CBG14881 [...	98	7e-20	
gi 55632563 ref XP_520343.1	PREDICTED: similar to bromodom...	91	1e-17	
gi 28573564 ref NP_611401.2	CG7229-PA [Drosophila melanoga...	86	3e-16	G
gi 16604681 qb AAL24133.1	putative kinase [Arabidopsis tha...	86	3e-16	G
gi 19528087 qb AAL90158.1	AT24439p [Drosophila melanogaster]	86	3e-16	
gi 7573452 emb CAE87766.1	kinase-like protein [Arabidopsis...	86	3e-16	

gi 9294219 db BAB02121.1	unnamed protein product [Arabido...	85	6e-16	
gi 15232127 ref NP_189362.1	DNA-binding bromodomain-contai...	85	6e-16	G
gi 4581512 emb CAE40169.1	SPCC1450.02 [Schizosaccharomyces...	84	8e-16	
gi 46438562 gb EAK97891.1	hypothetical protein Ca019.8593 ...	84	1e-15	
gi 47201045 emb CAF89147.1	unnamed protein product [Tetrao...	84	1e-15	
gi 27803968 gb AAO22056.1	IMB1 [Arabidopsis thaliana] >gi ...	83	2e-15	G
gi 3033396 gb AAC12830.1	putative RING3 protein [Arabidops...	83	2e-15	
gi 42571057 ref NP_973602.1	DNA-binding bromodomain-contai...	83	2e-15	G
gi 20259928 gb AAM13311.1	unknown protein [Arabidopsis tha...	83	2e-15	
gi 56236042 gb AAV84477.1	At1g73150 [Arabidopsis thaliana]...	82	4e-15	G
gi 50253452 gb AAF71928.1	At5g63330 [Arabidopsis thaliana]...	81	7e-15	G
gi 50940753 ref XP_479904.1	putative bromodomain-containsin...	80	2e-14	G
gi 19114532 ref NP_593620.1	protein with 2 bromodomains, p...	80	2e-14	G
gi 17551634 ref NP_508124.1	kinase (40.9 kD) (XB213) [Caen...	79	3e-14	G
gi 57282320 emb CAD43286.1	bromodomain-containing RNA-bind...	79	3e-14	
gi 49652967 emb CAG85306.1	unnamed protein product [Debary...	79	3e-14	G
gi 7671448 emb CAB89388.1	bromodomain protein-like [Arabid...	79	3e-14	G
gi 19173489 ref NP_597292.1	GENERAL TRANSCRIPTION FACTOR [...	79	3e-14	G
gi 39592569 emb CAE63646.1	Hypothetical protein CBG08144 [...	79	3e-14	
gi 13186138 emb CAC33451.1	PSTVd RNA-binding protein, Virpl...	79	4e-14	
gi 34874095 ref XP_221050.2	similar to fetal Alzheimer ant...	78	6e-14	G
gi 54635558 gb EAL24961.1	GA15830-PA [Drosophila pseudoobs...	78	6e-14	
gi 57282318 emb CAD43285.1	bromodomain-containing RNA-bind...	78	6e-14	
gi 57090969 ref XP_537586.1	PREDICTED: similar to fetal Al...	78	7e-14	
gi 30046988 gb AAH50566.1	FALZ protein [Homo sapiens]	78	7e-14	G
gi 31322942 gb AAF22284.1	bromodomain PHD finger transcrip...	78	7e-14	G
gi 30793995 gb AAF40447.1	unknown protein [Arabidopsis tha...	78	7e-14	G
gi 55645849 ref XP_511643.1	PREDICTED: hypothetical protei...	78	7e-14	
gi 38788274 ref NP_872579.2	fetal Alzheimer antigen isoform...	78	7e-14	G
gi 38788260 ref NP_004450.3	fetal Alzheimer antigen isoform...	78	7e-14	G
gi 8978291 db BAA98182.1	unnamed protein product [Arabido...	78	7e-14	
gi 45595651 gb AAH67234.1	FALZ protein [Homo sapiens]	78	7e-14	G
gi 7428977 pir S71788	P/CAF protein - human	78	7e-14	
gi 6683492 db BAA89208.1	bromodomain PHD finger transcrip...	78	7e-14	G
gi 38174486 gb AAH60715.1	Falz protein [Mus musculus]	77	1e-13	G
gi 18204482 gb AAH21489.1	Falz protein [Mus musculus]	77	1e-13	G
gi 31216247 ref XP_316196.1	ENSANGP00000005931 [Anopheles ...	77	1e-13	G
gi 6016737 gb AAF01563.1	hypothetical protein [Arabidopsis...	77	1e-13	
gi 57282316 emb CAD43284.1	bromodomain-containing RNA-bind...	77	1e-13	
gi 51766499 ref XP_126724.5	fetal Alzheimer antigen [Mus m...	77	1e-13	G
gi 22136456 gb AAM91306.1	unknown protein [Arabidopsis tha...	77	1e-13	G
gi 24654644 ref NP_728507.1	CG32346-PA, isoform A [Drosoph...	77	1e-13	G
gi 24654638 ref NP_728505.1	CG32346-PB, isoform B [Drosoph...	77	1e-13	G
gi 57282322 emb CAD43287.1	bromodomain-containing RNA-bind...	77	1e-13	
gi 28516430 ref XP_284106.1	similar to PCAF acetyltransfer...	77	1e-13	G
gi 16265798 gb AAL16644.1	nucleosome remodeling factor lar...	77	1e-13	
gi 48104118 ref XP_395718.1	similar to fetal Alzheimer ant...	77	1e-13	G
gi 11359006 pir T42517	bromodomain protein - fission yeast...	77	1e-13	
gi 25406905 pir A86198	hypothetical protein [imported] - A...	77	1e-13	G
gi 40805843 ref NP_003875.3	p300/CBP-associated factor [Ho...	77	2e-13	G

gi 57103570 ref XP_534249.1 	PREDICTED: similar to p300/CBP...	77	2e-13	
gi 55619933 ref XP_516321.1 	PREDICTED: similar to p300/CBP...	77	2e-13	
gi 50937581 ref XP_478318.1 	putative RING3 protein [Oryza ...	77	2e-13	G
gi 23297757 gb AAN13019.1 	unknown protein [Arabidopsis tha...	77	2e-13	G
gi 50733046 ref XP_426001.1 	PREDICTED: similar to PCAF [Ga...	77	2e-13	G
gi 27574121 pdb 1N72 A	Chain A, Structure And Ligand Of A H...	77	2e-13	S
gi 25511645 pir H86312	F2H15.2 protein - Arabidopsis thali...	77	2e-13	
gi 14317910 dbj BAE59138.1 	PCAF [Gallus gallus]	77	2e-13	G
gi 34874275 ref XP_217321.2 	similar to PCAF acetyltransfer...	76	2e-13	G
gi 31209509 ref XP_313721.1 	ENSANGP00000003808 [Anopheles ...	76	2e-13	G
gi 34903950 ref NP_913322.1 	putative PSTVd RNA-binding prot...	76	2e-13	G
gi 49650060 emb CAG79786.1 	unnamed protein product [Yarrow...	76	2e-13	G
gi 47221861 emb CAF98873.1 	unnamed protein product [Tetrao...	76	2e-13	
gi 15810439 gb AAL07107.1 	unknown protein [Arabidopsis tha...	76	3e-13	
gi 57282314 emb CAD43283.1 	bromodomain-containing RNA-bind...	76	3e-13	
gi 50757845 ref XP_415674.1 	PREDICTED: similar to fetal Al...	76	3e-13	G
gi 435855 gb AAB28651.1 	CREB-binding protein; CBP [Mus sp....	75	4e-13	G
gi 737920 prf I1923401A	protein CBP	75	4e-13	
gi 47223942 emb CAG06119.1 	unnamed protein product [Tetrao...	75	5e-13	
gi 38099205 gb EAA46582.1 	hypothetical protein MG08925.4 [...	75	6e-13	G
gi 50345997 ref NP_001420.2 	E1A binding protein p300 [Homo...	74	8e-13	G
gi 3024341 sp Q09472 P300 HUMAN	E1A-associated protein p300...	74	8e-13	G
gi 6320132 ref NP_010213.1 	Protein involved in transcripti...	74	8e-13	G
gi 31753089 gb AAH53889.1 	EP300 protein [Homo sapiens]	74	8e-13	G
gi 57092731 ref XP_531721.1 	PREDICTED: similar to E1A-asso...	74	8e-13	
gi 56118232 ref NP_808489.3 	E1A binding protein p300 [Mus ...	74	8e-13	
gi 55661272 ref XP_515155.1 	PREDICTED: E1A binding protein...	74	8e-13	
gi 48094965 ref XP_394317.1 	similar to ENSANGP00000004748 ...	74	8e-13	G
gi 4321116 gb AAC51331.2 	CREB-binding protein [Homo sapiens]	74	1e-12	G
gi 6321691 ref NP_011768.1 	Histone acetyltransferase, acet...	74	1e-12	G
gi 38505359 gb AAR23149.1 	CREB-binding protein [Rattus nor...	74	1e-12	G
gi 57088067 ref XP_536991.1 	PREDICTED: similar to CREB-bin...	74	1e-12	
gi 4758056 ref NP_004371.1 	CREB binding protein [Homo sapi...	74	1e-12	G
gi 55249595 gb AAH86282.1 	Unknown (protein for MGC:83709) ...	74	1e-12	
gi 51769561 ref XP_148699.4 	CREB binding protein [Mus musc...	74	1e-12	G
gi 51769419 ref XP_489497.1 	similar to CREB-binding protei...	74	1e-12	G
gi 51013881 gb AAT93234.1 	YGR252W [Saccharomyces cerevisiae]	74	1e-12	
gi 50728690 ref XP_416238.1 	PREDICTED: similar to E1A-asso...	74	1e-12	G
gi 19547887 gb AAL87532.1 	CREB-binding protein [Mus muscul...	74	1e-12	G
gi 49117594 gb AAH72594.1 	Unknown (protein for IMAGE:64084...	74	1e-12	
gi 21307831 gb AAL54859.1 	CREB-binding protein [Aplysia ca...	74	1e-12	
gi 1502355 emb CAA67614.1 	GCN5 [Saccharomyces cerevisiae]	74	1e-12	
gi 47217876 emb CAG02369.1 	unnamed protein product [Tetrao...	74	1e-12	
gi 631119 pir S39162	transcription coactivator CREB-bindin...	74	1e-12	
gi 23200188 pdb 1JSP B	Chain B, Nmr Structure Of Cbp Bromod...	74	1e-12	S
gi 11513447 pdb 1E61 A	Chain A, Bromodomain From Gcn5 Compl...	74	1e-12	S
gi 24659254 ref NP_726307.1 	CG30417-PA [Drosophila melanog...	74	1e-12	G
gi 46227211 gb EAK88161.1 	protein with 4 ankyrin repeats p...	74	1e-12	
gi 50755982 ref XP_414964.1 	PREDICTED: similar to CREB-bin...	74	1e-12	G
gi 54636653 gb EAL35582.1 	hypothetical protein Chro.50328 ...	74	1e-12	

gi 5468533 gb AAC50890.2	p300/CBP-associated factor [Homo ...	74	1e-12	G
gi 44983942 gb AAS52978.1	AER297Cp [Ashbya gossypii ATCC 1...	73	2e-12	G
gi 52345413 ref NP_064389.2	p300/CBP-associated factor [Mu...	73	2e-12	G
gi 49649342 emb CAG79052.1	YlGCN5 [Yarrowia lipolytica CLI...	73	2e-12	G
gi 50287799 ref XP_446329.1	unnamed protein product [Candi...	73	2e-12	G
gi 7862148 gb AAF70498.1	PCAF acetyltransferase; p300/CBP-...	73	2e-12	G
gi 44983653 gb AAS52752.1	AER068Cp [Ashbya gossypii ATCC 1...	73	2e-12	G
gi 8885596 db SAA97526.1	unnamed protein product [Arabido...	73	2e-12	
gi 26451383 db BAC42791.1	unknown protein [Arabidopsis th...	73	2e-12	G
gi 54641233 gb EAL29983.1	GA16840-PA [Drosophila pseudoobs...	72	3e-12	
gi 50303459 ref XP_451671.1	unnamed protein product [Kluyv...	72	3e-12	G
gi 47229415 emb CAF99403.1	unnamed protein product [Tetrao...	72	4e-12	
gi 40744729 gb EAA63885.1	hypothetical protein AN1984.2 [A...	72	5e-12	G
gi 311664 emb CAA79377.1	BDF1 [Saccharomyces cerevisiae]	71	7e-12	
gi 608567 gb AAA89115.1	Bdflp	71	7e-12	
gi 6323431 ref NP_013503.1	Protein involved in transcripti...	71	7e-12	G
gi 31204369 ref XP_311133.1	ENSANGP00000004748 [Anopheles ...	71	7e-12	G
gi 24663348 ref NP_648586.2	CG4107-PA [Drosophila melanoga...	71	7e-12	G
gi 54642162 gb EAL30911.1	GA17962-PA [Drosophila pseudoobs...	71	7e-12	
gi 55243803 gb EAA06516.3	ENSANGP00000004748 [Anopheles ga...	71	7e-12	
gi 55243802 gb EAL41310.1	ENSANGP00000025904 [Anopheles ga...	71	7e-12	
gi 45383496 ref NP_989660.1	GCN5 general control of amino-...	71	7e-12	G
gi 50285717 ref XP_445287.1	unnamed protein product [Candi...	71	7e-12	G
gi 3211728 gb AAC39102.1	GCN5; HAT [Drosophila melanogaster]	71	7e-12	
gi 38099365 gb EAA46722.1	hypothetical protein MG09943.4 [...	71	7e-12	G
gi 39590738 emb CAE65110.1	Hypothetical protein CBG09974 [...	71	7e-12	
gi 47208228 emb CAF96470.1	unnamed protein product [Tetrao...	70	1e-11	
gi 54642704 gb EAL31449.1	GA13644-PA [Drosophila pseudoobs...	70	2e-11	
gi 19115719 ref NP_594807.1	putative yeast transcriptional...	70	2e-11	G
gi 17533491 ref NP_496998.1	bromodomain PHD finger transcr...	70	2e-11	G
gi 17533489 ref NP_496997.1	bromodomain PHD finger transcr...	70	2e-11	G
gi 17533487 ref NP_496996.1	bromodomain PHD finger transcr...	70	2e-11	G
gi 24640863 ref NP_524642.2	CG15319-PB [Drosophila melanog...	70	2e-11	G
gi 31432077 gb AAP53762.1	contains similarity to histone a...	70	2e-11	G
gi 54110963 emb CAH60782.1	Hypothetical protein F26H11.2g ...	70	2e-11	
gi 50507802 emb CAH04722.1	Hypothetical protein F26H11.2c ...	70	2e-11	
gi 34364498 emb CAB54234.3	Hypothetical protein F26H11.2d ...	70	2e-11	
gi 7499972 pir T21435	hypothetical protein F26H11.3c - Cae...	70	2e-11	
gi 26350027 db BAC38653.1	unnamed protein product [Mus mu...	69	3e-11	G
gi 29569106 gb AAO84020.1	global transcription factor grou...	69	3e-11	
gi 50302579 ref XP_451225.1	unnamed protein product [Kluyv...	69	3e-11	G
gi 12321252 gb AAG50696.1	hypothetical protein [Arabidopsi...	69	3e-11	G
gi 7511830 pir T13828	CREB-binding protein homolog - fruit...	69	4e-11	
gi 32400806 gb AAP80635.1	histone acetyltransferase [Triti...	68	6e-11	
gi 31711984 gb AAP68348.1	At3g54610 [Arabidopsis thaliana]...	68	6e-11	G
gi 7258364 emb CAB77581.1	histon acetyltransferase HAT1 [A...	68	6e-11	
gi 47226142 emb CAG04516.1	unnamed protein product [Tetrao...	68	6e-11	
gi 47218844 emb CAG02829.1	unnamed protein product [Tetrao...	68	6e-11	
gi 46433121 gb EAK92574.1	likely histone acetyltransferase...	68	8e-11	
gi 54638697 gb EAL28099.1	GA15159-PA [Drosophila pseudoobs...	68	8e-11	
gi 56468960 gb EAL46759.1	bromodomain protein, putative [E...	68	8e-11	

gi 55297001 db BAD68476.1	DNA-binding bromodomain-contain...	68	8e-11	
gi 24651761 ref NP_536734.2	CG1966-PA [Drosophila melanoga...	67	1e-10	G
gi 57228236 gb AAW44693.1	conserved hypothetical protein [...	67	1e-10	
gi 31224454 ref XP_317442.1	ENSANGP00000011787 [Anopheles ...	67	1e-10	G
gi 50256825 gb EAL19543.1	hypothetical protein CNBG1720 [C...	67	1e-10	
gi 55237658 gb EAA12387.2	ENSANGP00000011787 [Anopheles ga...	67	1e-10	
gi 16768864 gb AAL28651.1	LD09043p [Drosophila melanogaster]	67	1e-10	
gi 68563666 gb AAF29981.1	histone acetyltransferase GCN5 [T...	67	1e-10	
gi 5031520 gb AAD38202.1	histone acetyltransferase GCN5 [T...	67	1e-10	
gi 5059246 gb AAD38952.1	ATP-dependent chromatin assembly ...	67	1e-10	
gi 38105685 gb EAA52082.1	hypothetical protein MG03677.4 [...	67	1e-10	G
gi 7635502 emb CAB88669.1	chromatin accessibility complex ...	67	1e-10	
gi 13183793 gb AAK15343.1	CECR2 protein [Homo sapiens] >gi...	67	1e-10	G
gi 17552708 ref NP_499161.1	CBP/p300 homolog (cbp-1) [Caen...	67	1e-10	G
gi 17552710 ref NP_499160.1	CBP/p300 homolog (cbp-1) [Caen...	67	1e-10	G
gi 52545926 emb CAH56122.1	hypothetical protein [Homo sapi...	67	1e-10	G
gi 2133462 pir S60123	hypothetical protein R10E11.1 - Caen...	67	1e-10	
gi 12698025 db BAB21831.1	KIAA1740 protein [Homo sapiens]	67	1e-10	G
gi 33242492 gb AAQ00945.1	general control nonrepressed 5 [...	67	2e-10	
gi 57106607 ref XP_534935.1	PREDICTED: similar to Cat eye ...	67	2e-10	
gi 50910201 ref XP_466589.1	putative global transcription ...	67	2e-10	G
gi 51979260 ref XP_507492.1	PREDICTED OJ1791_B03.42-1 gene...	67	2e-10	G
gi 13699186 db BAB41205.1	kinase-like protein [Oryza sativa]	67	2e-10	
gi 17017400 gb AAL33654.1	histone acetyl transferase [Zea ...	66	2e-10	
gi 50729022 ref XP_416392.1	PREDICTED: similar to KIAA1740...	66	2e-10	G
gi 50728910 ref XP_416340.1	PREDICTED: similar to Transcri...	66	2e-10	G
gi 48105414 ref XP_393011.1	similar to CG32394-PA [Apis me...	66	2e-10	G
gi 40740639 gb EAA59829.1	conserved hypothetical protein [...	65	4e-10	G
gi 51717063 ref XP_204234.3	cat eye syndrome chromosome re...	65	4e-10	G
gi 51714476 ref XP_489839.1	similar to Cat eye syndrome cr...	65	4e-10	G
gi 10045561 emb CAC07919.1	putative protein [Arabidopsis t...	65	4e-10	G
gi 17534715 ref NP_494767.1	bromodomain adjacent zinc fing...	65	5e-10	G
gi 49658230 emb CAG91071.1	unnamed protein product [Debary...	65	5e-10	G
gi 47230592 emb CAF99785.1	unnamed protein product [Tetrao...	65	5e-10	
gi 2267585 gb AAB63585.1	transcription intermediary factor...	65	5e-10	G
gi 998813 gb AAB34289.1	TIF1 [Mus sp.]	65	6e-10	G
gi 42546847 gb EAA69690.1	conserved hypothetical protein [...	65	6e-10	G
gi 34391523 gb AAN61105.1	putative chromatin remodelling f...	65	6e-10	G
gi 32417982 ref XP_329469.1	hypothetical protein [Neurospo...	65	6e-10	G
gi 34328067 ref NP_659542.1	tripartite motif protein 24 [M...	65	6e-10	G
gi 56473058 gb EAL50506.1	bromodomain protein, putative [E...	65	6e-10	
gi 38110007 gb EAA55792.1	hypothetical protein MG01443.4 [...	65	6e-10	G
gi 19343832 gb AAH25482.1	Trim24 protein [Mus musculus]	65	6e-10	G
gi 51094800 gb EAL24046.1	transcriptional intermediary fac...	64	8e-10	G
gi 51094801 gb EAL24047.1	transcriptional intermediary fac...	64	8e-10	G
gi 55629844 ref XP_519502.1	PREDICTED: transcriptional int...	64	8e-10	
gi 47211977 emb CAF95299.1	unnamed protein product [Tetrao...	64	8e-10	
gi 32420965 ref XP_330926.1	hypothetical protein [Neurospo...	64	1e-09	G
gi 25058961 gb AAH39907.1	GCN5 general control of amino-ac...	64	1e-09	G

gi 34873737 ref XP_239340.2	similar to GCN5 general contro...	64	1e-09	G
gi 57091497 ref XP_548094.1	PREDICTED: similar to GCN5 gen...	64	1e-09	
gi 31204491 ref XP_311194.1	ENSANGP00000001532 [Anopheles ...	64	1e-09	G
gi 55645415 ref XP_511500.1	PREDICTED: similar to GCN5 gen...	64	1e-09	G
gi 10835101 ref NP_066564.1	GCN5 general control of amino-...	64	1e-09	G
gi 39795334 gb AAH63752.1	General control of amino acid sy...	64	1e-09	G
gi 37811671 gb AAP03834.1	general control of amino-acid sy...	64	1e-09	
gi 1911495 gb AAB50690.1	hGCN5=transcriptional adaptor [hu...	64	1e-09	
gi 13278322 gb AAH03983.1	Gcn5l2 protein [Mus musculus]	64	1e-09	G
gi 12084461 pdb 1F68 A	Chain A, Nmr Solution Structure Of T...	64	1e-09	
gi 46228118 gb EAK89017.1	GCN5 like acetylase + bromodoma...	63	2e-09	
gi 54658191 gb EAL36865.1	histone acetyltransferase [Crypt...	63	2e-09	
gi 48094754 ref XP_392182.1	similar to ENSANGP00000020172 ...	63	2e-09	G
gi 1245146 gb AAB01099.1	HAT A1	63	2e-09	
gi 51979535 ref XP_507560.1	PREDICTED P0007D08.15 gene pro...	63	2e-09	G
gi 28829334 gb AAO51876.1	similar to Dictyostelium discoid...	63	2e-09	
gi 31210237 ref XP_314085.1	ENSANGP00000003691 [Anopheles ...	62	3e-09	G
gi 34911780 ref NP_917237.1	OJ1316_H05.17 [Oryza sativa (j...	62	3e-09	G
gi 9910238 ref NP_064388.1	general control of amino acid s...	62	3e-09	G
gi 55240574 gb EAA09379.3	ENSANGP00000003691 [Anopheles ga...	62	3e-09	
gi 55296880 db BAD58333.1	PSTVd RNA-binding protein-like [...	62	3e-09	
gi 29248585 gb EAA40115.1	GLP_80_20751_21473 [Giardia lamb...	62	3e-09	
gi 14165484 gb AAH08039.1	BRD8 protein [Homo sapiens] >gi ...	62	5e-09	G
gi 34452709 ref NP_899203.1	bromodomain containing 8 isofo...	62	5e-09	G
gi 21536234 ref NP_084423.1	bromodomain containing 8 [Mus ...	62	5e-09	G
gi 34452707 ref NP_631938.1	bromodomain containing 8 isofo...	62	5e-09	G
gi 2135974 pir S68142	probable transcription factor SMAP -...	62	5e-09	G
gi 42554923 gb EAA77766.1	hypothetical protein FG09717.1 [...	62	5e-09	G
gi 57093561 ref XP_531918.1	PREDICTED: similar to bromodom...	62	5e-09	
gi 56606080 ref NP_001008509.1	bromodomain containing 8 [R...	62	5e-09	
gi 34452705 ref NP_006687.3	bromodomain containing 8 isofo...	62	5e-09	G
gi 18606031 gb AAH23160.1	Brd8 protein [Mus musculus]	62	5e-09	G
gi 55732238 emb CAH92823.1	hypothetical protein [Pongo pyg...	62	5e-09	
gi 2707336 gb AAB92257.1	histone acetyltransferase [Arabid...	62	5e-09	
gi 2655006 gb AAB87858.1	thyroid hormone receptor coactiva...	62	5e-09	G
gi 57525007 ref NP_001006148.1	similar to bromodomain cont...	61	7e-09	
gi 34854705 ref XP_229225.2	similar to KIAA1476 protein [R...	61	7e-09	G
gi 50754923 ref XP_414542.1	PREDICTED: similar to bromodom...	61	7e-09	G
gi 53136534 emb CAG32596.1	hypothetical protein [Gallus ga...	61	7e-09	G
gi 26328143 db BAC27812.1	unnamed protein product [Mus mu...	61	7e-09	G
gi 57222786 gb AAW40830.1	transcriptional activator gcn5, ...	61	9e-09	
gi 50261018 gb EAL23668.1	hypothetical protein CNBA3150 [C...	61	9e-09	
gi 54635725 gb EAL25128.1	GA10623-PA [Drosophila pseudoobs...	61	9e-09	
gi 57097415 ref XP_532754.1	PREDICTED: similar to transcri...	60	1e-08	
gi 55238947 gb EAL40012.1	ENSANGP00000029642 [Anopheles ga...	60	1e-08	
gi 19074752 ref NP_586258.1	TRANSCRIPTIONAL ACTIVATOR [Enc...	60	2e-08	G
gi 27503567 gb AAH42646.1	BC053917 protein [Mus musculus]	60	2e-08	G
gi 46433516 gb EAK92953.1	potential chromatin-associated p...	60	2e-08	
gi 56472259 gb EAL49757.1	bromodomain protein, putative [E...	60	2e-08	
gi 56468123 gb EAL46008.1	bromodomain protein, putative [E...	60	2e-08	
gi 15778343 gb AAL07393.1	CECR2B [Homo sapiens]	60	2e-08	G

gi 56518510 emb CAH76159.1	histone acetyltransferase Gcn5,...	59	3e-08	
gi 56499474 emb CAH95151.1	histone acetyltransferase Gcn5,...	59	3e-08	
gi 24370476 emb CAC70157.1	polybromodomain protein [Brugia...	59	3e-08	
gi 24370475 emb CAC70156.1	polybromodomain protein [Brugia...	59	3e-08	
gi 23491055 gb EAA22686.1	similar to S. cerevisiae BDF1 [P...	59	3e-08	
gi 23490365 gb EAA22160.1	histone acetyltransferase GCN5-r...	59	3e-08	
gi 38503467 gb AAR22527.1	histone acetyltransferase [Plasm...	59	4e-08	
gi 23612782 ref NP_704321.1	histone acetyltransferase Gcn5...	59	4e-08	G
gi 7304923 ref NP_038478.1	bromodomain adjacent to zinc fi...	59	4e-08	G
gi 46098556 gb EAK83789.1	hypothetical protein UM02619.1 [...	59	4e-08	
gi 45382753 ref NP_990008.1	extracellular matrix protein F...	59	4e-08	G
gi 29421196 dbj BAA96000.2	KIAA1476 protein [Homo sapiens]	59	4e-08	G
gi 47220585 emb CAG05611.1	unnamed protein product [Tetrao...	59	4e-08	
gi 39598267 emb CAF68959.1	Hypothetical protein CBG14939 [...	59	4e-08	
gi 5262644 emb CAB45759.1	hypothetical protein [Homo sapie...	59	4e-08	G
gi 22653668 sp Q9UIF8 BA2B HUMAN	Bromodomain adjacent to zi...	59	4e-08	G
gi 55612288 ref XP_525949.1	PREDICTED: bromodomain adjacen...	59	5e-08	
gi 23508131 ref NP_700801.1	hypothetical protein PF10_0328...	58	6e-08	G
gi 56472529 gb EAL50010.1	bromodomain protein, putative [E...	58	6e-08	
gi 46226948 gb EAK87914.1	chromodomain-helicase-DNA-bindin...	58	6e-08	
gi 54657614 gb EAL36361.1	RIKEN cDNA A730019I05 gene [Cryp...	58	6e-08	
gi 54657612 gb EAL36360.1	hypothetical protein Chro.20286 ...	58	8e-08	
gi 45551085 ref NP_725062.2	CG10897-PB, isoform B [Drosoph...	57	1e-07	G
gi 24652776 ref NP_725061.1	CG10897-PD, isoform D [Drosoph...	57	1e-07	G
gi 24652774 ref NP_725060.1	CG10897-PC, isoform C [Drosoph...	57	1e-07	G
gi 22023997 ref NP_523701.2	CG10897-PA, isoform A [Drosoph...	57	1e-07	G
gi 12642598 gb AAK00302.1	Toutatis [Drosophila melanogaster]	57	1e-07	
gi 56501185 emb CAH98647.1	hypothetical protein PB001232.0...	57	1e-07	
gi 26326149 dbj BAC26818.1	unnamed protein product [Mus mu...	57	1e-07	G
gi 57228880 gb AAW45314.1	conserved hypothetical protein [...	57	1e-07	
gi 57087477 ref XP_536845.1	PREDICTED: similar to bromodom...	57	1e-07	
gi 50256505 gb EAL19230.1	hypothetical protein CNBH3290 [C...	57	1e-07	
gi 47086497 ref NP_997942.1	Unknown (protein for MGC:66249...	57	1e-07	G
gi 56474427 gb EAL51797.1	bromodomain protein, putative [E...	57	1e-07	
gi 28277586 gb AAH44181.1	Brd8 protein [Danio rerio]	57	1e-07	G
gi 19113148 ref NP_596356.1	putative transcriptional activ...	57	2e-07	G
gi 50749002 ref XP_426440.1	PREDICTED: similar to bromodom...	57	2e-07	G
gi 47211530 emb CAF90136.1	unnamed protein product [Tetrao...	57	2e-07	
gi 20357588 ref NP_620278.1	TBP-associated factor 1 isofo...	56	2e-07	G
gi 34865213 ref XP_234156.2	similar to chromatin remodelin...	56	2e-07	G
gi 20357585 ref NP_004597.2	TBP-associated factor 1 isofo...	56	2e-07	G
gi 34481757 emb CAD70493.2	putative DYT3 protein [Homo sap...	56	2e-07	G
gi 34481755 emb CAD70492.2	putative DYT3 protein [Homo sap...	56	2e-07	G
gi 34481753 emb CAD70491.2	putative DYT3 protein [Homo sap...	56	2e-07	G
gi 34481733 emb CAD87527.1	putative DYT3 protein [Homo sap...	56	2e-07	G
gi 47214801 emb CAF89628.1	unnamed protein product [Tetrao...	56	2e-07	
gi 47206036 emb CAF91716.1	unnamed protein product [Tetrao...	56	2e-07	
gi 47205952 emb CAF90865.1	unnamed protein product [Tetrao...	56	2e-07	
gi 39582716 emb CAF65922.1	Hypothetical protein CBG11090 [...	56	2e-07	
gi 8569258 pdb 1EQF A	Chain A, Crystal Structure Of The Dou...	56	2e-07	
gi 14670392 ref NP_115784.1	bromodomain adjacent to zinc f...	56	3e-07	G

gi 17510001 ref NP_491173.1	histone acetyltransferase (88....	56	3e-07	G
gi 57112471 ref XP_549070.1	PREDICTED: similar to TBP-asso...	56	3e-07	
gi 31198613 ref XP_308254.1	ENSANGP00000010809 [Anopheles ...	56	3e-07	G
gi 6683496 db BAA89210.1	bromodomain adjacent to zinc fin...	56	3e-07	G
gi 33589500 gb AAQ22517.1	LD26355p [Drosophila melanogaster]	56	3e-07	
gi 24649782 ref NP_651288.1	CG11375-PA [Drosophila melanog...	56	3e-07	G
gi 55639437 ref XP_509537.1	PREDICTED: similar to KIAA0314...	56	3e-07	
gi 55628708 ref XP_527780.1	PREDICTED: hypothetical protei...	56	3e-07	
gi 55245294 gb EAL41745.1	ENSANGP000000028929 [Anopheles ga...	56	3e-07	
gi 55245293 gb EAA03942.2	ENSANGP000000010809 [Anopheles ga...	56	3e-07	
gi 48103752 ref XP_395639.1	similar to ENSANGP00000003310 ...	56	3e-07	G
gi 4165087 gb AAD08675.1	Williams-Beuren syndrome deletion...	56	3e-07	G
gi 47223904 emb CAG06081.1	unnamed protein product [Tetrao...	56	3e-07	
gi 32967603 ref NP_038476.2	bromodomain adjacent to zinc f...	55	4e-07	G
gi 26338768 db BAC33055.1	unnamed protein product [Mus mu...	55	4e-07	G
gi 34881239 ref XP_228551.2	similar to CCG1 [Rattus norveg...	55	4e-07	G
gi 57090081 ref XP_537409.1	PREDICTED: similar to bromodom...	55	4e-07	
gi 6683494 db BAA89209.1	bromodomain adjacent to zinc fin...	55	4e-07	G
gi 24659555 ref NP_729188.1	CG32394-PA [Drosophila melanog...	55	4e-07	G
gi 32967605 ref NP_872589.1	bromodomain adjacent to zinc f...	55	4e-07	G
gi 28958186 gb AAH47418.1	B430306D02Rik protein [Mus muscu...	55	4e-07	G
gi 51772243 ref XP_194622.4	similar to CCG1 [Mus musculus]	55	4e-07	G
gi 51767276 ref XP_484142.1	hypothetical protein B930060C0...	55	4e-07	G
gi 4884108 emb CAB43261.1	hypothetical protein [Homo sapie...	55	4e-07	G
gi 40787763 gb AAH65123.1	BC065123 protein [Mus musculus]	55	4e-07	G
gi 22653665 sp Q9NRL2 BA1A HUMAN	Bromodomain adjacent to zi...	55	4e-07	G
gi 26338285 db BAC32828.1	unnamed protein product [Mus mu...	55	4e-07	G
gi 19075972 ref NP_588472.1	putative transcriptional regul...	55	5e-07	G
gi 42549961 gb EAA72804.1	hypothetical protein FG04423.1 [...	55	5e-07	G
gi 24020884 gb AAN40840.1	TBP-associated factor RNA polyme...	55	5e-07	G
gi 50760409 ref XP_418009.1	PREDICTED: similar to Transcri...	55	5e-07	G
gi 50745680 ref XP_420198.1	PREDICTED: similar to CCG1 [Ga...	55	5e-07	G
gi 42558222 db BAD11104.1	SNF2-family ATP dependent chrom...	55	5e-07	
gi 47209254 emb CAF91993.1	unnamed protein product [Tetrao...	55	5e-07	
gi 56202868 emb CAI21897.1	tripartite motif-containing 33 ...	55	7e-07	
gi 20129741 ref NP_610266.1	CG1845-PA [Drosophila melanoga...	55	7e-07	G
gi 34876969 ref XP_240329.2	similar to polybromo-1D [Rattu...	55	7e-07	G
gi 57098727 ref XP_533013.1	PREDICTED: similar to Transcri...	55	7e-07	
gi 30721853 gb AAP34197.1	polybromo-1D [Homo sapiens]	55	7e-07	G
gi 14971411 ref NP_148980.1	tripartite motif-containing 33...	55	7e-07	G
gi 12083896 gb AAG48941.1	polybromo-1 [Homo sapiens] >gi 4...	55	7e-07	G
gi 12083894 gb AAG48940.1	polybromo-1 [Homo sapiens] >gi 4...	55	7e-07	G
gi 12083892 gb AAG48939.1	polybromo-1 [Homo sapiens] >gi 3...	55	7e-07	G
gi 12083875 gb AAG48933.1	polybromo-1 [Homo sapiens]	55	7e-07	G
gi 54635374 gb EAL24777.1	GA14940-PA [Drosophila pseudoobs...	55	7e-07	
gi 51768295 ref XP_484357.1	RIKEN 2310032M22 [Mus musculus]	55	7e-07	G
gi 46097809 gb EAK83042.1	hypothetical protein UM05168.1 [...	55	7e-07	
gi 30794368 ref NP_060783.2	polybromo 1 [Homo sapiens] >gi...	55	7e-07	G
gi 16551971 db BAB71210.1	unnamed protein product [Homo s...	55	7e-07	G

gi 4325109 gb AAD17259.1	transcriptional intermediary fact...	55	7e-07	G
gi 27803071 emb CAD60774.1	unnamed protein product [Podosp...	55	7e-07	
gi 26326785 dbj EAC27136.1	unnamed protein product [Mus mu...	55	7e-07	G
gi 26365296 dbj BAB26374.2	unnamed protein product [Mus mu...	55	7e-07	G
gi 6755993 ref NP_035844.1	bromodomain adjacent to zinc fi...	54	9e-07	G
gi 50417257 gb AAH78299.1	Zgc:100857 protein [Danio rerio]	54	9e-07	G
gi 26332264 dbj BAC29862.1	unnamed protein product [Mus mu...	54	9e-07	G
gi 56202867 emb CAI21896.1	tripartite motif-containing 33 ...	54	1e-06	
gi 32421217 ref XP_331052.1	hypothetical protein [Neurospo...	54	1e-06	G
gi 55620429 ref XP_516515.1	PREDICTED: similar to polybrom...	54	1e-06	
gi 55587792 ref XP_513668.1	PREDICTED: tripartite motif-co...	54	1e-06	
gi 14971413 ref NP_056990.2	tripartite motif-containing 33...	54	1e-06	G
gi 56202866 emb CAI21895.1	tripartite motif-containing 33 ...	54	1e-06	
gi 5834582 emb CAB55313.1	rfg7 protein [Homo sapiens]	54	1e-06	G
gi 5689563 dbj BAA03065.1	KIAA1113 protein [Homo sapiens]	54	1e-06	G
gi 45384026 ref NP_990496.1	polybromo 1 protein [Gallus ga...	54	1e-06	G
gi 38197516 gb AAH08965.2	BAZ2A protein [Homo sapiens]	54	1e-06	G
gi 57092555 ref XP_538237.1	PREDICTED: similar to hypothet...	54	1e-06	
gi 37194693 gb AAH58241.1	Unknown (protein for IMAGE:63083...	54	1e-06	
gi 7304921 ref NP_038477.1	bromodomain adjacent to zinc fi...	54	1e-06	G
gi 14670390 ref NP_075381.2	bromodomain adjacent to zinc f...	54	1e-06	G
gi 54648598 gb AAH84946.1	Unknown (protein for IMAGE:49603...	54	1e-06	
gi 33469025 ref NP_473419.1	bromodomain adjacent to zinc f...	54	1e-06	G
gi 37360250 dbj BAC98103.1	mKIAA1113 protein [Mus musculus]	54	1e-06	G
gi 46229766 gb EAK90584.1	protein with 2 bromo domains [Cr...	54	1e-06	
gi 54657810 gb EAL36527.1	hypothetical protein Chro.70137 ...	54	1e-06	
gi 51476484 emb CAH18232.1	hypothetical protein [Homo sapi...	54	1e-06	
gi 28972143 dbj BAC65525.1	mKIAA0314 protein [Mus musculus]	54	1e-06	G
gi 4049922 gb AAC97879.1	transcription factor WSTF [Homo s...	54	1e-06	G
gi 56490889 emb CAI05770.1	hypothetical protein PB301534.0...	54	1e-06	
gi 22653669 sp Q9UIF9 BA2A HUMAN	Bromodomain adjacent to zi...	54	1e-06	G
gi 2224569 dbj BAA20773.1	KIAA0314 [Homo sapiens]	54	1e-06	G
gi 474971 dbj BAA05110.1	CCG1 [Mesocricetus auratus] >gi 2...	53	2e-06	
gi 34867725 ref XP_221627.2	similar to WDR9 protein, form ...	53	2e-06	G
gi 34862191 ref XP_222315.2	similar to TTF-I interacting p...	53	2e-06	G
gi 57108950 ref XP_544889.1	PREDICTED: similar to WD-repea...	53	2e-06	
gi 55643327 ref XP_523285.1	PREDICTED: similar to CREB-bin...	53	2e-06	
gi 37360534 dbj BAC98245.1	mKIAA1740 protein [Mus musculus]	53	2e-06	G
gi 57229792 gb AAW46194.1	nucleus protein, putative [Crypt...	53	3e-06	
gi 23508824 ref NP_701492.1	bromodomain protein, putative ...	53	3e-06	G
gi 45433503 ref NP_444400.1	tripartite motif protein 33 [M...	53	3e-06	G
gi 50255361 gb EAL18096.1	hypothetical protein CNBK1170 [C...	53	3e-06	
gi 54637438 gb EAL26840.1	GAL0956-PA [Drosophila pseudoobs...	53	3e-06	
gi 51770163 ref XP_196171.4	bromodomain and PHD finger con...	53	3e-06	G
gi 55962792 emb CAI11773.1	novel protein [Danio rerio]	53	3e-06	
gi 37360308 dbj BAC98132.1	mKIAA1286 protein [Mus musculus]	53	3e-06	G
gi 56518079 emb CAH79038.1	bromodomain protein, putative [...]	53	3e-06	
gi 56515560 emb CAH84003.1	hypothetical protein PC300805.0...	53	3e-06	
gi 23480253 gb EAA16864.1	ERYTHROCYTE MEMBRANE PROTEIN PFE...	53	3e-06	

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|15706263|emb|CAC69989.1| ☒ bromodomain containing 2 [Homo sapiens]
Length = 801

Score = 217 bits (553), Expect = 6e-56
Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60
YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE
Sbjct: 81 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 140

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP
Sbjct: 141 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 181

Score = 100 bits (248), Expect = 1e-20
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY
Sbjct: 368 YAWPFYKPVDSALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCYK 427

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101
YN P D+V MA+ L+ +F + A MP
Sbjct: 428 YNPPDHDVVAMARKLQDVFEFRYAKMP 454

☐ >gi|4826806|ref|NP_005095.1| ☒ bromodomain containing protein 2 [Homo sapiens]
gi|56207529|emb|CAI18689.1| bromodomain containing 2 [Homo sapiens]
gi|56206429|emb|CAI18548.1| bromodomain containing 2 [Homo sapiens]
gi|55961972|emb|CAI18110.1| bromodomain containing 2 [Homo sapiens]
gi|55961413|emb|CAI17492.1| bromodomain containing 2 [Homo sapiens]
gi|2980663|emb|CAA43996.1| ☒ FSH [Homo sapiens]
gi|52545950|emb|CAH56171.1| ☒ hypothetical protein [Homo sapiens]
gi|577293|db|BAA07641.1| ☒ KIAA9001 [Homo sapiens]
gi|12230989|sp|P25440|BRD2 HUMAN ☒ Bromodomain-containing protein 2 (RING3 protei
Length = 801

Score = 217 bits (553), Expect = 6e-56
Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60
YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE
Sbjct: 81 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 140

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP
Sbjct: 141 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 181

Score = 100 bits (248), Expect = 1e-20
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY
Sbjct: 368 YAWPFYKPVDAALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCYK 427

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101
YN P D+V MA+ L+ +F + A MP
Sbjct: 428 YNPPDHDVVAMARKLQDVFEFRIYAKMP 454

>gi|1082363|pir||A56619 female sterile homeotic (fsh) homolog RING3 - human
gi|182769|gb|AAA68890.1| G putative
Length = 754

Score = 217 bits (553), Expect = 6e-56
Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60
YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE
Sbjct: 34 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 93

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP
Sbjct: 94 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 134

Score = 100 bits (248), Expect = 1e-20
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY
Sbjct: 321 YAWPFYKPVDAALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCYK 380

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101
YN P D+V MA+ L+ +F + A MP
Sbjct: 381 YNPPDHDVVAMARKLQDVFEFRIYAKMP 407

>gi|51770504|ref|XP_489783.1| G similar to MMRING3.1.2 [Mus musculus]
gi|3811391|gb|AAC69907.1| G RING3 [Mus musculus]
gi|2995270|emb|CAA15819.1| MMRING3.1.2-[Mus musculus]
gi|3041763|dbj|BAA25416.1| G Ring3 [Mus musculus]
Length = 798

Score = 217 bits (553), Expect = 6e-56
Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60
YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE
Sbjct: 80 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 139

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101

CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP

Sbjct: 140 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 180

Score = 100 bits (248), Expect = 1e-20

Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74


+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY

Sbjct: 367 YAWPFYKPVDAALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCYK 426

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101

YN P D+V MA+ L+ +F + A MP

Sbjct: 427 YNPPDHDVVAMARKLQDVFEFRYAKMP 453

 >gi|57094404|ref|XP_532103.1| PREDICTED: similar to Bromodomain-containing protein (O27.1.1) [Canis familiaris]
Length = 800

Score = 217 bits (553), Expect = 6e-56

Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60

YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE

Sbjct: 99 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 158

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101

CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP

Sbjct: 159 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 199

Score = 100 bits (248), Expect = 1e-20

Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74




+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY

Sbjct: 365 YAWPFYKPVDAALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCYK 424

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101

YN P D+V MA+ L+ +F + A MP

Sbjct: 425 YNPPDHDVVAMARKLQDVFEFRYAKMP 451

 >gi|47059183|ref|NP_997660.1|  bromodomain-containing 2 [Rattus norvegicus]
gi|46237556|emb|CAE83937.1|  bromodomain-containing 2 [Rattus norvegicus]
Length = 798

Score = 217 bits (553), Expect = 6e-56

Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60

YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE




Sbjct: 80 YLHKVVMKALWKHQFAWPFRQPVDVAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 139

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP
Sbjct: 140 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 180

Score = 100 bits (248), Expect = 1e-20
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY
Sbjct: 367 YAWPFYKPVDA SALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCYK 426

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101
YN P D+V MA+ L+ +F + A MP
Sbjct: 427 YNPPDHDVVAMARKLQDVFEFRYAKMP 453

 >[gi|6753910|ref|NP_034368.1|](#)  bromodomain containing 2 [Mus musculus]
[gi|3273701|gb|AAC24810.1|](#)  female sterile homeotic-related protein Frg-1 [Mus mu]
Length = 798

Score = 217 bits (553), Expect = 6e-56
Identities = 101/101 (100%), Positives = 101/101 (100%)


Query: 1 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60
YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE
Sbjct: 80 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 139

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP
Sbjct: 140 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 180

Score = 100 bits (248), Expect = 1e-20
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY
Sbjct: 367 YAWPFYKPVDA SALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCYK 426

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101
YN P D+V MA+ L+ +F + A MP
Sbjct: 427 YNPPDHDVVAMARKLQDVFEFRYAKMP 453

 >[gi|55956582|emb|CAI11405.1|](#) bromodomain-containing protein 2 [Canis familiaris]
Length = 803

Score = 217 bits (553), Expect = 6e-56
Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60
YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE
Sbjct: 81 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 140

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101
 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP
 Sbjct: 141 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 181

Score = 100 bits (248), Expect = 1e-20
 Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74
 +AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY
 Sbjct: 368 YAWPFYKPVDA SALGLHDYHDI IKHPMDLSTV KRKMENRDYRDAQEFAADVRLMFSNCYK 427

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101
 YN P D+V MA+ L+ +F + A MP
 Sbjct: 428 YNPPDHDVVAMARKLQDVFEFRYAKMP 454

>gi|55725298|emb|CAH89514.1| hypothetical protein [Pongo pygmaeus]
 Length = 546

Score = 217 bits (553), Expect = 6e-56
 Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE 60
 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE
 Sbjct: 81 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE 140

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101
 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP
 Sbjct: 141 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 181

Score = 100 bits (248), Expect = 1e-20
 Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74
 +AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY
 Sbjct: 368 YAWPFYKPVDA SALGLHDYHDI IKHPMDLSTV KRKMENRDYRDAQEFAADVRLMFSNCYK 427

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101
 YN P D+V MA+ L+ +F + A MP
 Sbjct: 428 YNPPDHDVVAMARKLQDVFEFRYAKMP 454

>gi|52545923|emb|CAH56179.1| hypothetical protein [Homo sapiens]
 Length = 754

Score = 217 bits (553), Expect = 6e-56
 Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE 60
 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE
 Sbjct: 34 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE 93



Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101

CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP
 Sbjct: 94 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 134

Score = 100 bits (248), Expect = 1e-20
 Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74
 +AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY
 Sbjct: 321 YAWPFYKPVDA SALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCYK 380

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101
 YN P D+V MA+ L+ +F + A MP
 Sbjct: 381 YNPPDHDVVAMARKLQDVFEFRYAKMP 407

 >gi|12802523|gb|AAK07919.1|  ring 3 [Mus musculus]
 Length = 503

Score = 217 bits (553), Expect = 6e-56
 Identities = 101/101 (100%), Positives = 101/101 (100%)



Query: 1 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE 60
 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE
 Sbjct: 80 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE 139

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101
 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP
 Sbjct: 140 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 180

Score = 100 bits (248), Expect = 1e-20
 Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74
 +AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY
 Sbjct: 367 YAWPFYKPVDA SALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCYK 426

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101
 YN P D+V MA+ L+ +F + A MP
 Sbjct: 427 YNPPDHDVVAMARKLQDVFEFRYAKMP 453

 >gi|1370115|emb|CAA65450.1|  kinase [Homo sapiens]
 Length = 754

Score = 217 bits (553), Expect = 6e-56
 Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE 60
 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE
 Sbjct: 34 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE 93

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101
 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP

Sbjct: 94 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 134

Score = 100 bits (248), Expect = 1e-20
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY
Sbjct: 321 YAWPFYKPVDAALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCYK 380

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101
YN P D+V MA+ L+ +F + A MP
Sbjct: 381 YNPPDHDVVAMARKLQDVFEFRYAKMP 407

 >gi|2995269|emb|CAA15818.1|  MMRING3.1.1 [Mus musculus]
Length = 752

Score = 217 bits (553), Expect = 6e-56
Identities = 101/101 (100%), Positives = 101/101 (100%)




Query: 1 YLHKVVMKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60
YLHKVVMKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE
Sbjct: 34 YLHKVVMKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 93

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP
Sbjct: 94 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 134

Score = 100 bits (248), Expect = 1e-20
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY
Sbjct: 321 YAWPFYKPVDAALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCYK 380

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101
YN P D+V MA+ L+ +F + A MP
Sbjct: 381 YNPPDHDVVAMARKLQDVFEFRYAKMP 407

 >gi|2780779|dbj|BAA24379.1|  Ring3 [Mus musculus]
gi|2780777|dbj|BAA24378.1|  Ring3 [Mus musculus]
Length = 503

Score = 217 bits (553), Expect = 6e-56
Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60
YLHKVVMKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE
Sbjct: 34 YLHKVVMKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 93



Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP

Sbjct: 94 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 134

Score = 100 bits (248), Expect = 1e-20
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY
Sbjct: 321 YAWPFYKPVDAALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCYK 380

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101
YN P D+V MA+ L+ +F + A MP
Sbjct: 381 YNPPDHDVVAMARKLQDVFEFRYAKMP 407

 >gi|2780775|dbj|BAA24377.1|  Ring3 [Mus musculus]
Length = 549

Score = 217 bits (553), Expect = 6e-56
Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60
YLHKVVMKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE
Sbjct: 80 YLHKVVMKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 139

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP
Sbjct: 140 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 180

Score = 100 bits (248), Expect = 1e-20
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY
Sbjct: 367 YAWPFYKPVDAALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNCYK 426

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101
YN P D+V MA+ L+ +F + A MP
Sbjct: 427 YNPPDHDVVAMARKLQDVFEFRYAKMP 453

 >gi|39645317|gb|AAH63840.1|  BRD2 protein [Homo sapiens]
Length = 836

Score = 217 bits (553), Expect = 6e-56
Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60
YLHKVVMKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE
Sbjct: 81 YLHKVVMKALWKHQFAWPFRQPVDAVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 140

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP
Sbjct: 141 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 181

Score = 100 bits (248), Expect = 1e-20
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY
Sbjct: 368 YAWPFYKPVDASALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNICY 427

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101
YN P D+V MA+ L+ +F + A MP
Sbjct: 428 YNPPDHDVVAMARKLQDVFEFRYAKMP 454

>gi|1588281|prf|2208296A RING3 protein
Length = 509

Score = 217 bits (553), Expect = 6e-56
Identities = 101/101 (100%), Positives = 101/101 (100%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60
YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE
Sbjct: 34 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 93

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP
Sbjct: 94 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 134

Score = 100 bits (248), Expect = 1e-20
Identities = 46/87 (52%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74
+AWPF +PVDA LGL DYH IIK PMD+ T+KR++EN Y A E D MF+NCY
Sbjct: 203 YAWPFYKPVDASALGLHDYHDIKHPMDLSTVKKRMENRDYRDAQEFAADVRLMFSNICY 262

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101
YN P D+V MA+ L+ +F + A MP
Sbjct: 263 YNPPDHDVVAMARKLQDVFEFRYAKMP 289

>gi|1370092|emb|CAA65449.1| kinase [Gallus gallus]
Length = 729

Score = 213 bits (542), Expect = 1e-54
Identities = 98/101 (97%), Positives = 99/101 (98%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWAASE 60
YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYW A+E
Sbjct: 34 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPMDMGTIKRRLENNYYWGAAE 93

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVA MP
Sbjct: 94 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVAQMP 134

Score = 100 bits (250), Expect = 8e-21
Identities = 47/87 (54%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74
+AWPF +PVDA LGL DYH+IIK PMD+ TIKR++EN Y A E D MF+NCY
Sbjct: 315 YAWPFYKPVDASALGLHDYHEIIKHPMDLSTIKRKMENRDYHDAQEFAADVRLMFSNCK 374

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101
YN P D+V MA+ L+ +F A MP
Sbjct: 375 YNPPDHDVVAMARKLQDVFEFSYAKMP 401

>gi|3129967|emb|CAA18965.1| RING3 kinase [synthetic construct]
gi|7512236|pir|T28145 RING3 kinase - chicken
Length = 733

Score = 213 bits (542), Expect = 1e-54
Identities = 98/101 (97%), Positives = 99/101 (98%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE 60
YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYW A+E
Sbjct: 34 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWGAAE 93

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVA MP
Sbjct: 94 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVAQMP 134

Score = 100 bits (250), Expect = 8e-21
Identities = 47/87 (54%), Positives = 58/87 (66%)

Query: 15 FAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASECMQDFNTMFTNCYI 74
+AWPF +PVDA LGL DYH+IIK PMD+ TIKR++EN Y A E D MF+NCY
Sbjct: 319 YAWPFYKPVDASALGLHDYHEIIKHPMDLSTIKRKMENRDYHDAQEFAADVRLMFSNCK 378

Query: 75 YNKPTDDIVLMAQTLEKIFLQKVASMP 101
YN P D+V MA+ L+ +F A MP
Sbjct: 379 YNPPDHDVVAMARKLQDVFEFSYAKMP 405

>gi|34392374|dbj|BAC82511.1| Serine threonine Kinase [Coturnix japonica]
Length = 735

Score = 213 bits (542), Expect = 1e-54
Identities = 98/101 (97%), Positives = 99/101 (98%)

Query: 1 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWAASE 60
YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYW A+E
Sbjct: 34 YLHKVVMKALWKHQFAWPFRQPVD AVKLGLPDYHKIIKQPM DMGTIKRRLENNYYWGAAE 93

Query: 61 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVASMP 101
CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVA MP
Sbjct: 94 CMQDFNTMFTNCYIYNKPTDDIVLMAQTLEKIFLQKVAQMP 134